

FIG. 4

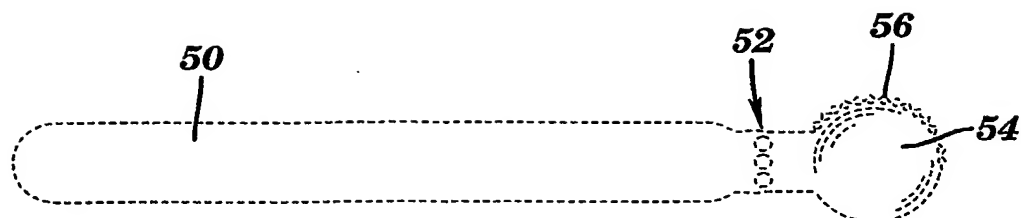


FIG. 5A

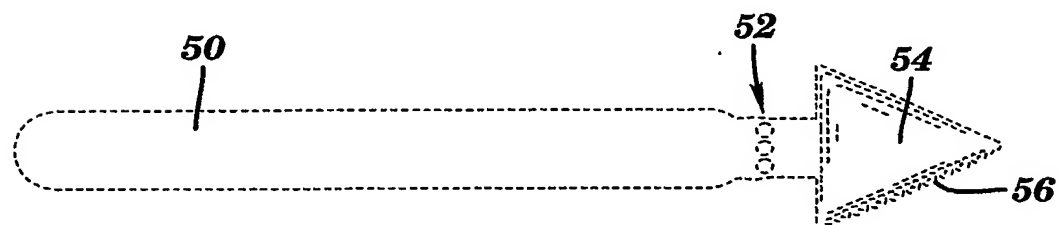


FIG. 5B

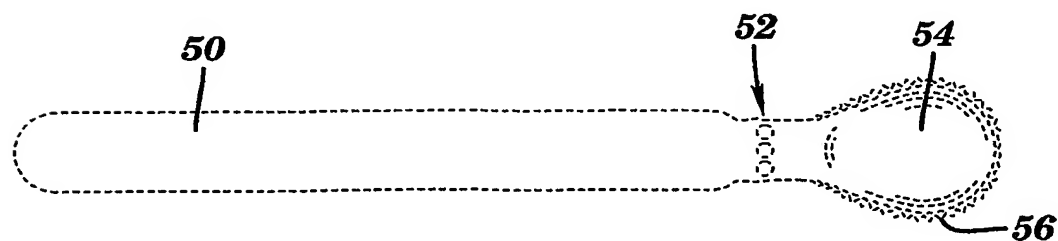
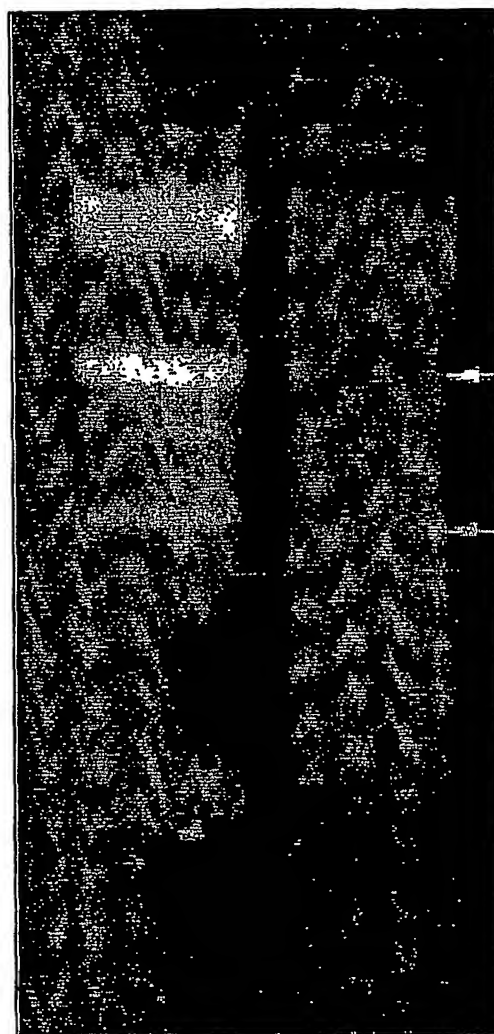


FIG. 5C



LANE 1

LANE 2

FIG. 6

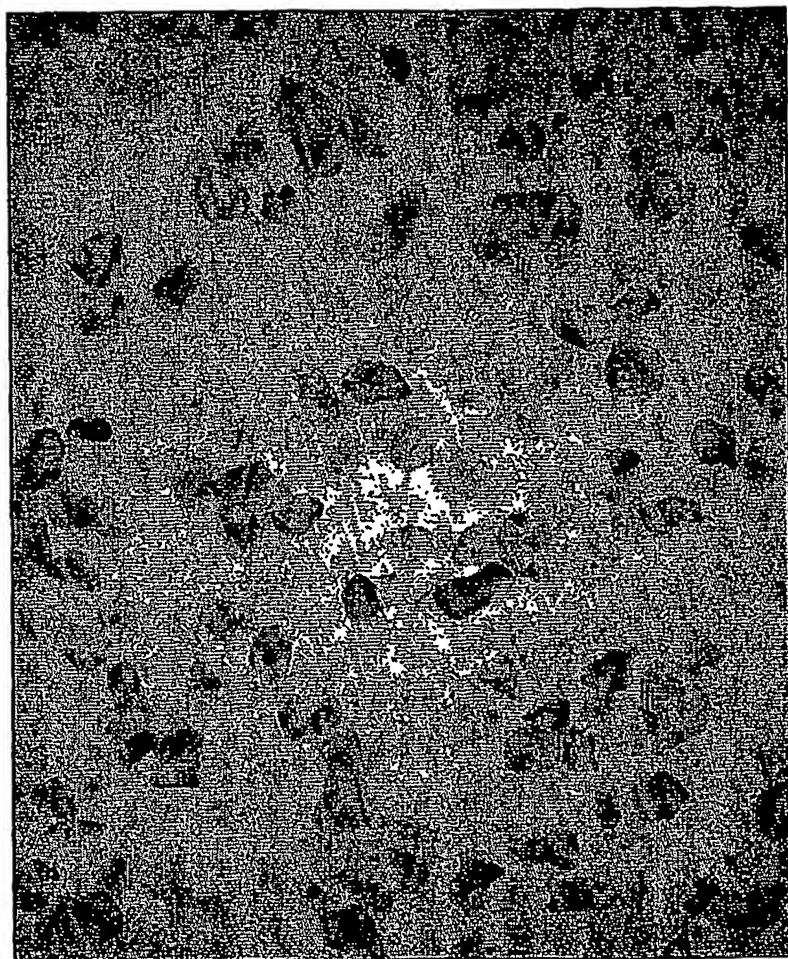
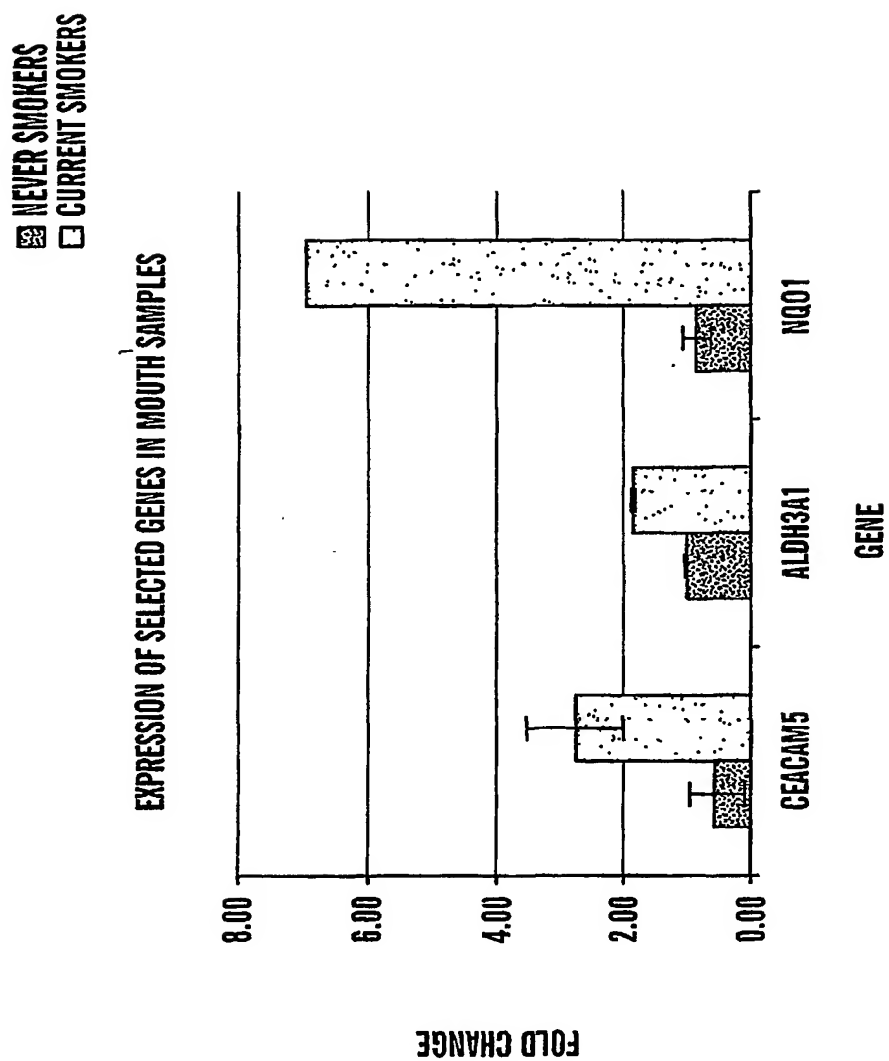
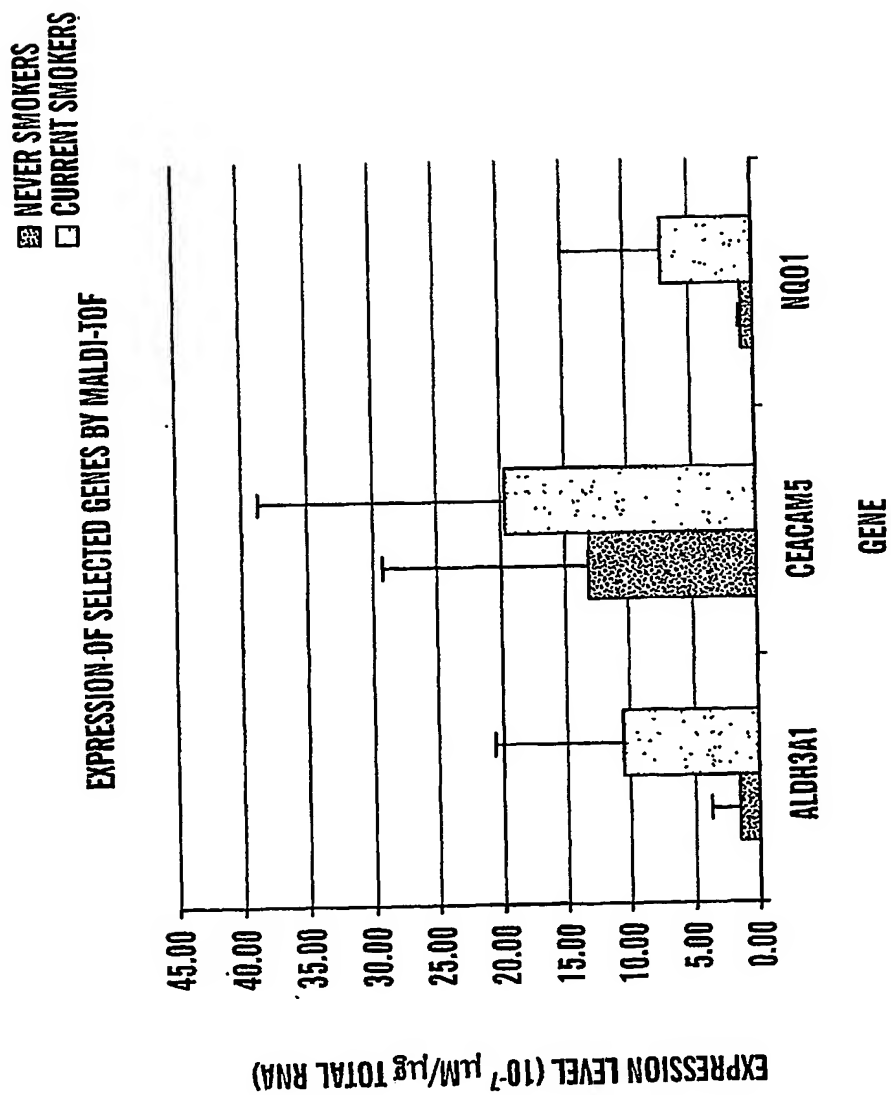


FIG. 7

**FIG. 8A**

**FIG. 8B**

- NEVER SMOKERS (MOUTH - MASS SPEC)
- NEVER SMOKERS (AIRWAY - ARRAY)
- CURRENT SMOKERS (MOUTH - MASS SPEC)
- CURRENT SMOKERS (AIRWAY - ARRAY)

CORRELATING GENE EXPRESSION BETWEEN AIRWAY AND MOUTH

CURRENT VS NEVER SMOKERS; ARRAY VS MASS SPEC TECHNOLOGY

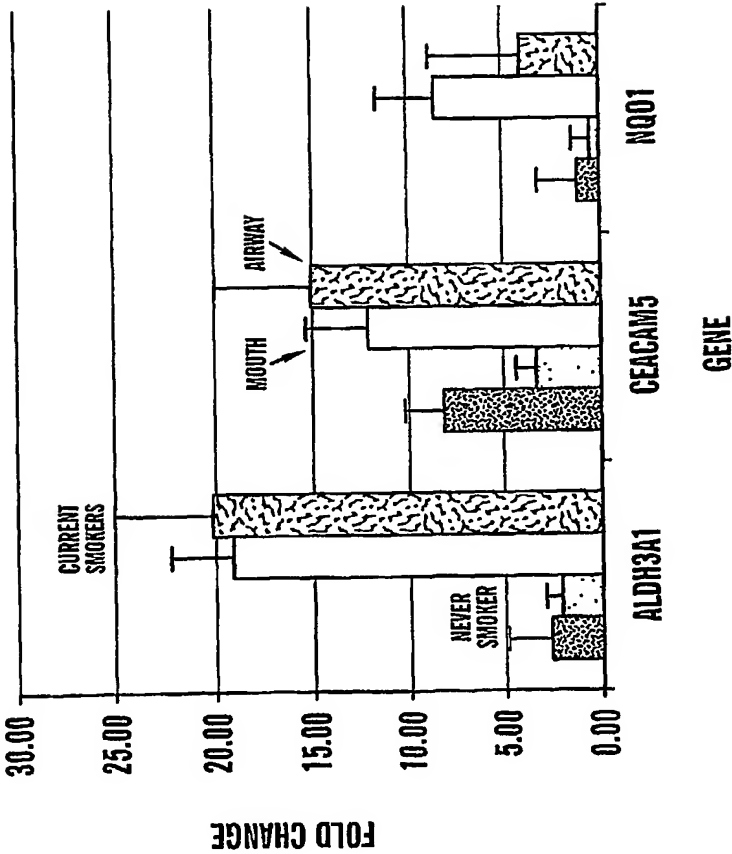


FIG. 9

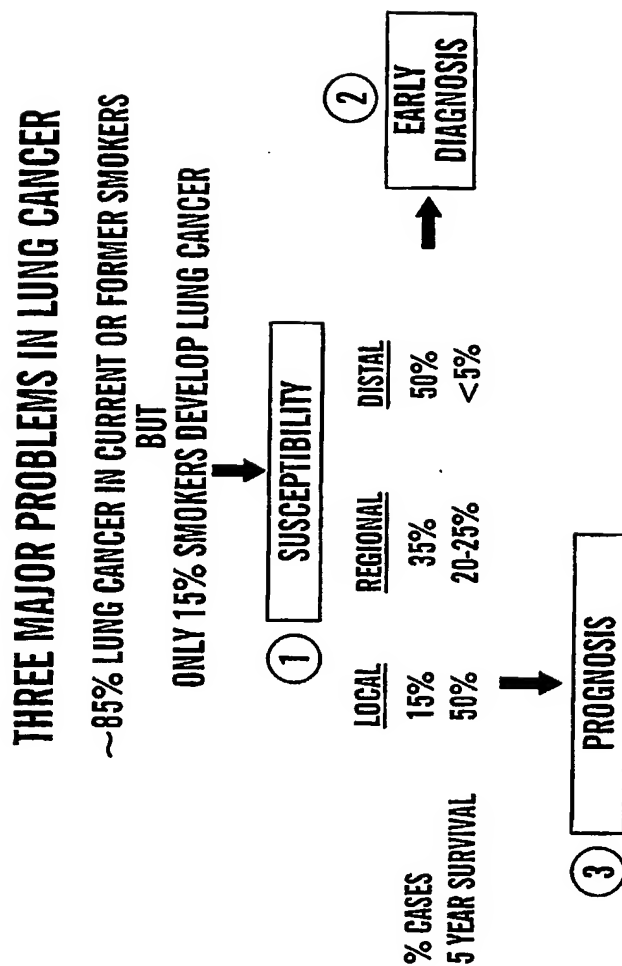


FIG. 10

Affymetrix ID	GENBANK ID	HUGO ID	GO ID	Current/Never smoker p-value	Current/Never smoker Ratio	CHROMOSOME LOCATION	GENBANK DESCRIPTION
220562_at	NM_017781.1	FLJ20359	6118	1.2E-05	0.414665	7p22.3	hypothetical protein FLJ20359
219410_at	NM_018004.1	FLJ10134	16021	0.00044	0.435962	3q12.3	hypothetical protein FLJ10134
	AF078844.1	MT1F	5737	2.4E-05	0.469865	16q13	metallothionein 1F (functional)
	NM_005951.1	MT1H	46872	3.4E-05	0.481306	16q13	metallothionein 1H
	BC005894.1	FMO2	6118	0.0005	0.487651	1q23-q25	flavin containing monooxygenase 2
	AF182275.1	CYP2A6	6118	0.00041	0.509566	19q13.2	"cytochrome P450, family 2, subfamily A, polypeptide 6"
	BE246115	MT1F	5737	1.7E-07	0.523748	16q13	metallothionein 1F (functional)
	NM_005952.1	MT1X	9634	6.3E-06	0.546094	16q13	metallothionein 1X
	NM_005950.1	MT1G	46872	1.8E-06	0.554828	16q13	metallothionein 1G
	NM_001823.1	CKB	5737	0.00079	0.567052	14q32	"creatine kinase, brain"
	NM_000860.1	HPGD	8152	0.00061	0.569176	4q34-q35	hydroxyprostaglandin dehydrogenase 15-(NAD) integral membrane
	AL021786	ITM2A	16021	7.1E-05	0.578361	Xq13.3-Xq21.2	protein 2A
	L29008.1	SORD	6060	0.00036	0.580542	15q15.3	sorbitol dehydrogenase
	NM_002275.1	KRT15	8544	0.00056	0.581235	17q21.2	keratin 15
	AF333388.1	na		3.9E-05	0.585312	1q42.3	hypothetical gene supported by S68948
	U56725.1	HSPA2	7286	4.2E-07	0.586718	14q24.1	heat shock 70kDa protein 2
	M10943	MT1F	5737	5.1E-07	0.596388	16q13	metallothionein 1F (functional)

FIG. 11

396_f_at	BF217861	MT1E	6823	0.00038	0.596821	16q13	metallothionein 1E (functional)
	AF052094.1	EPAS1		1.5E-05	0.613378	2p21-p16	endothelial PAS domain protein 1 erythropoietin receptor
	X97671	EPOR	7165	0.00035	0.614894	19p13.3-p13.2	metallothionein 1X
	NM_002450.1	MT1X	5737	2.3E-06	0.631575	16q13	"tumor necrosis factor (ligand) superfamily, member 13"
205752_s_at	AF114012.1	TNFSF13		2.3E-05	0.674117	17p13.1	metallothionein 2A
	NM_005953.1	MT2A	6878	5E-05	0.675192	16q13	tensin
	AL046979	TNS		0.00018	0.679047	2q35-q36	glutathione
	NM_000851.1	GSTM5	6803	0.00019	0.688656	1p13.3	S-transferase M5 peroxisomal
	AB017546	PEX14	5777	0.00045	0.696156	1p36.22	biogenesis factor 14
	NM_006312.1	NCOR2	3677	3.3E-05	0.703316	12q24	nuclear receptor co-repressor 2
							connector enhancer of KSR-like
	NM_006314.1	CNK1	7242	0.00069	0.706868	1p35.3	(Drosophila kinase suppressor of ras)
	AB014605.1	AIP1	7242	0.00093	0.716147	7q21	atrophin-1 interacting protein 1
							"transcription factor 7-like 1 (T-cell specific, HMG-box)"
	NM_031283.1	TCF7L1	6355	1.3E-05	0.719296	2p11.2	HMG-box"
	AB007857	KIAA0397		0.00019	0.721366	17p13.3	KIAA0397 gene product
	NM_001888.1	CRYM	7601	0.00085	0.727149	16p13.11-p12.3	"crystallin, mu" carbohydrate
	NM_005769.1	CHST4	8146	0.00095	0.73709	16q22.2	(N-acetylglucosamine 6-O)

FIG. 11
(cont'd.)

BC006230.1	MGLL	6954	6.3E-06	0.739267	3q21.3	sulfotransferase 4
NM_018555.2	ZNF463	6355	0.00041	0.753755	19q13.3-q13.4	monoglyceride lipase
						zinc finger protein 463
						SMART/HDAC1
						associated repressor
NM_015001.1	SHARP	3676	0.00016	0.766024	1p36.33-p36.11	protein
NM_016605.1	C5orf6	5634	0.00032	0.795545	5q31	chromosome 5 open
						reading frame 6
						"golgi associated,
						gamma adaptin ear
						containing, ARF
AW001443	GGA1	6886	0.00097	0.799768	22q13.31	binding protein 1"
AA046650	HRIHFB2122	30047	0.00047	0.806466	22q13.1	Tara-like protein
						KDEL (Lys-Asp-Glu-Leu)
Z97056	KDEL3		0.00088	0.835711	22q13.1	endoplasmic reticulum
						protein retention receptor 3
BC001049.1	UFD1L	6511	0.0007	1.198875	22q11.21	ubiquitin fusion
						degradation 1-like
NM_015523.1	DKFZP566E144	9117	5.2E-05	1.200265	11q23.1-q23.2	small fragment
NM_006694.1	JTB	7048	0.00044	1.201571	1q21	nuclease
NM_030796.1	DKFZP564K0822		0.00043	1.209285	7p11.2	jumping translocation
AF217514.1	C20orf11		0.00014	1.219712	20q13.11	breakpoint
AF027205.1	SPINT2	6928	0.00063	1.220877	19q13.1	hypothetical protein
						DKFZp564K0822
						chromosome 20 open
						reading frame 111
						"serine protease inhibitor,
						Kunitz type, 2"
						hypothetical protein
						from clone 643
BC003379.1	LOC57228		0.00051	1.223881	12q13.13	guanylate kinase 1
BC006249.1	GUK1	6183	9.2E-05	1.234086	1q32-q41	chromosome 1
NM_004872.1	C1orf8	16021	0.00057	1.242047	1p36-p31	

FIG. 11
(cont'd.)

209679_s_at

M94859.1	CANX	9306	0.00038	1.243131	5q35	open reading frame 8 calnexin "FK506 binding protein 1A, 12kDa" hypothetical protein LOC92482 "CAP, adenylate cyclase-associated protein 1 (yeast)" DKFZP434J214 protein ribophorin II protein expressed in thyroid sequestosome 1 "proteasome (prosome, macropain) subunit, beta type, 5" "thioredoxin-like, 32kDa" "transducin-like enhancer of split 1 (E(sp1) homolog, Drosophila)" "signal sequence receptor, delta (translocon-associated protein delta)" thioredoxin domain containing 5 "coatmer protein complex, subunit
NM_000801.1	FKBP1A	6457	0.00038	1.247517	20p13	
AV706096	LOC92482	6915	0.00019	1.248195	10q25.3	
NM_006367.2	CAP1	7190	0.00052	1.256141	1p34.2	
AL556438	DKFZP434J214		0.00097	1.257122	3q25.31	
BC003560.1	RPN2	6464	0.00045	1.257736	20q12-q13.1	
NM_014297.1	YF13H12		0.0002	1.260627	19q13.32	
NM_003900.1	SQSTM1	5829	0.00012	1.264144	5q35	
BC004146.1	PSMB5		3.3E-05	1.265493	14q11.2	
NM_004786.1	TXNL	7165	0.0002	1.270987	18q21.31	
AI951720	TLE1	6355	0.00031	1.272507	9q21.32	
NM_006280.1	SSR4	6886	0.00024	1.273482	Xq28	
NM_030810.1	TXNDC5	6118	0.00074	1.275599	6p24.3	
NM_004766.1	COPB2	6886	6.4E-05	1.278174	3q23	

FIG. 11
(cont'd.)

AF139131.1	BECN1	6916	0.00087	1.28931	17q21	beta 2 (beta prime)" "beclin 1 (coiled-coil, myosin-like BCL2 interacting protein)" transmembrane trafficking protein tumor rejection antigen (gp96) 1 UDP-N-acetyl-alpha- D-galactosamine: polypeptide N- acetylglucosaminyltransferase 1 (GalNAc-T1) katanin p80 (WD repeat containing) subunit B 1 hypothetical protein MGC4342 tight junction protein 2 (zona occludens 2) calcium binding protein P22 chromosome 6 open reading frame 80 Down syndrome critical region gene 5 "proteasome (prosome, macropain) 26S subunit, non-ATPase, 14" tumor-associated calcium signal transducer 2 "ubiquitin-conjugating
NM_006827.1	TMP21	6888	0.00047	1.296788	14q24.3	
NM_003299.1	TRA1	5524	3.1E-05	1.299298	12q24.2-q24.3	
NM_020474.2	GALNT1	7157	4.3E-05	1.300002	18q12.1	
NM_005886.1	KATNB1	7049	0.00034	1.301892	16q13	
NM_024329.1	MGC4342	5509	0.00028	1.304455	1p36.13	
NM_004817.1	TJP2	7242	0.00096	1.306517	9q13-q21	
AK000095.1	CHP		0.00084	1.311387	15q13.3	
BC000758.1	C6orf80		0.00015	1.318101	6q23.1-q24.1	
AB035745.1	DSCR5	16021	0.00033	1.321519	21q22.2	
NM_005805.1	PSMD14	6511	0.00067	1.333381	2q24.3	
J04152	TACSTD2	8283	0.00037	1.335595	1p32-p31	
NM_016021.1	UBE2J1	4840	0.00029	1.336642	6q16.1	

217823_s_at

FIG. 11
(cont'd.)

213135_at	BG054844 BC001709.1	ARHE FLJ13052	7012	0.00018 2.1E-05	1.402285 1.404051	2q23.3 1p36.33-p36.21	(amyloidosis, Finnish type)" "ras homolog gene family, member E" NAD kinase T-cell lymphoma invasion and metastasis 1 "histone 1, H2bk" "Homo sapiens histone 1, H2ac, mRNA (cDNA clone IMAGE:6526471), partial cds" "solute carrier family 17 (anion/sugar transporter), member 5" "actin related protein 2/3 complex, subunit 3, 21kDa" yeast Sec31p homolog copine III cyclin G2 desmoglein 2 "protein tyrosine phosphatase type IVA, member 1" "UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 5" NAD kinase ATP/GTP binding protein 1 "procollagen-proline, 2-oxoglutarate 4-dioxygenase
	U90902.1 BC000893.1	TIAMI HIST1H2BK	6334	7.1E-05 0.00032	1.417117 1.425082	21q22.11 6p21.33	
	AL353759	---	7001	0.0004	1.428349	---	
221041_s_at	NM_012434.1	SLC17A5	6820	7.1E-05	1.428655	6q14-q15	
	AF004561.1 NM_014933.1 NM_003909.1 AW134535 BF031829	ARPC3 KIAA0905 CPNE3 CCNG2 DSG2	6928 6629 7049	0.00013 0.00016 0.00019 0.00013 0.00064	1.431352 1.432349 1.439945 1.444115 1.450408	12q24.11 4q21.3 8q21.2 4q21.22 18q12.1	
200733_s_at	U48296.1	PTP4A1	7048	5.3E-05	1.450813	6q12	
208918_s_at 204500_s_at	NM_004776.1 BC001709.1 NM_015239.1	B4GALT5 FLJ13052 AGTPBP1	5794	0.00028 2.1E-06 7.3E-05	1.454948 1.455424 1.466039	20q13.1-q13.2 1p36.33-p36.21 9q22.1	
	J02783.1	P4HB	6118	0.00011	1.472842	17q25	

FIG. 11
(cont'd.)

202554_s_at	NM_020672.1	SI00A14	5509	0.00017	1.479972	1q21.1	(proline 4-hydroxylase), beta polypeptide (protein disulfide isomerase; thyroid hormone binding protein p55)"
	AL527430	GSTM3	6803	0.00099	1.481409	1p13.3	S100 calcium binding protein A14 glutathione S-transferase M3 (brain) short-chain
	NM_004753.1	SDR1	8152	1E-08	1.49171	1p36.1	dehydrogenase/reductase 1 abhydrolase domain containing 2 "ATP-binding cassette, sub-family C (CFTR/MRP), member 1" "RAB2, member RAS oncogene family" lysophospholipase I "ferritin, heavy polypeptide 1" "RAP1, GTPase activating protein 1" diaphanous homolog 2 (Drosophila) PTB domain adaptor protein CED-6 sterol carrier protein 2 UDP-N-acetyl-alpha- D-galactosamine: polypeptide N- acetyl-galactos
	NM_007011.1	ABHD2	16021	8.8E-07	1.4988	15q26.1	
	AI539710	ABCC1	6832	9.7E-07	1.511282	16p13.1	
	NM_002865.1 BG288007	RAB2 LYPLA1	6886	0.00024 0.00058	1.528634 1.542594	8q12.1 8q11.23	
	NM_002032.1	FTH1	6826	1E-08	1.545805	11q13	
	NM_002885.1	RAP1GA1	7165	6.7E-05	1.549434	1p36.1-p35	
	NM_006729.1	DIAPH2		2.2E-05	1.549995	Xq22	
	AF200715.1 BC005911.1	CED-6 SCP2	6911 6694	0.00088 0.00044	1.555117 1.562614	2q32.3-q33 1p32	
203911_at	BF063271	GALNT3	5975	2.4E-06	1.575931	2q24-q31	

FIG. 11
(cont'd.)

204970_s_at	NM_002359.1 NM_005980.1	MAFG S100P	6355 5515	1.2E-07 2.8E-06	1.704793 1.712088	17q25 4p16	1 family, polypeptide A10" v-maf musculoaponeurotic fibrosarcoma oncogene homolog G (avian) S100 calcium binding protein P "cytochrome P450, family 4, subfamily F, polypeptide 3" peroxiredoxin 1 "S100 calcium binding protein A10 (annexin II ligand, calpactin I, light polypeptide (p11))" "UDP glycosyltransferase 1 family, polypeptide A10" UDP-N-acetyl-alpha-D- galactosamine:polypeptide N-acetylgalactosaminyltransferase 7 (GalNAc-T7) "glutamate-cysteine ligase, catalytic subunit" "GDP-mannose 4,6- dehydratase" hematological and neurological expressed 1 "ferritin, heavy polypeptide 1" hypothetical gene supported by AK057191; AL117536 connective tissue growth factor annexin A3
206515_at	NM_000896.1 L19184.1	CYP4F3 PRDX1	6118 8283	0.00038 7.7E-07	1.745995 1.760529	19p13.2 1p34.1	
	NM_002966.1	S100A10	7165	1.2E-05	1.765162	1q21	
	NM_021027.1	UGT1A10	8152	0	1.769976	2q37	
	NM_017423.1	GALNT7	5975	6E-08	1.772633	4q31.1	
	BF676980	GCLC	6534	1.7E-05	1.782371	6p12	
	NM_001500.1	GMDS	5975	5.4E-06	1.821792	6p25	
217755_at	NM_016185.1 AA083483	HN1 FTH1		9E-08 1.1E-05	1.842243 1.848912	17q25.2 11q13	
	AL117536.1	na		1.4E-05	1.875907	Xq28	
209369_at	M92934.1 M63310.1	CTGF ANXA3	1558 5737	2.8E-06 2.5E-07	1.907245 1.922919	6q23.1 4q13-q22	

FIG. 11
(cont'd.)

203963_at	NM_000463.1	UGT1A10	16758	1E-08	1.977759	2q37	"UDP glycosyltransferase
	NM_001218.2	CA12	6730	0	2.054255	15q22	1 family, polypeptide A10"
219928_s_at	NM_012189.1	CABYR	8603	1.7E-05	2.069324	18q11.2	carbonic anhydrase XII
	BC005008.1	CEACAM6	7165	6.1E-05	2.09128	19q13.2	calcium-binding tyrosine-
	NM_003330.1	TXNRD1	6118	3E-08	2.091704	12q23-q24.1	(Y)-phosphorylation regulated
	NM_002631.1	PGD	9051	9E-08	2.09455	1p36.3-p36.13	(fibrousheatin 2)
	NM_002061.1	GCLM	6534	2.6E-07	2.132184	1p22.1	carcinoembryonic antigen-related
	NM_006755.1	TALDO1	5975	0	2.147132	11p15.5-p15.4	cell adhesion molecule 6
22184i_s_at	M18728.1	CEACAM6	7165	1.5E-07	2.167528	19q13.2	(non-specific cross reacting antigen)
	NM_005213.1	CSTA	4869	0.00033	2.168054	3q21	thioredoxin reductase 1
	U73945.1	DEFB1	6805	0.00049	2.185117	8p23.2-p23.1	phosphogluconate
	AF313911.1	TXN	7165	0	2.209985	9q31	dehydrogenase
205499_at	BF514079	KLF4	5737	9.3E-06	2.247407	9q31	"glutamate-cysteine ligase,
	NM_006470.1	TRIM16	6118	3E-08	2.279802	17p11.2	modifier subunit"
	NM_014467.1	SRPUL	6099	0	2.330972	Xq21.33-q23	transaldolase 1
204058_at	AL049699	MEI	6099	1E-08	2.410897	6q12	carcinoembryonic
	NM_002395.2	MEI	6099	0	2.718782	6q12	antigen-related cell
							adhesion molecule 6
							(non-specific cross
							reacting antigen)
							cystatin A (stefin A)
							"defensin, beta 1"
							thioredoxin
							Kruppel-like
							factor 4 (gut)
							tripartite motif-
							containing 16
							sushi-repeat protein
							"malic enzyme 1,
							NADP(+)-dependent,
							cytosolic"
							"malic enzyme 1,

FIG. 11
(cont'd.)

209351_at	BC002690.1	KRT14	7148	0.00058	2.8239	17q12-q21	NADP(+)-dependent, cytosolic"
209386_at	A1346835	TM4SF1	5887	0.00012	2.998073	3q21-q25	"keratin 14 (epidermolysis bullosa simplex, Dowling-Meara, Koebner)"
							transmembrane 4 superfamily member 1
							"aldo-keto reductase family 1, member C1 (dihydrodiol dehydrogenase 1; 20-alpha (3-alpha)-hydroxysteroid dehydrogenase)"
	NM_001353.2	AKR1C1	6805	2.9E-05	3.186574	10p15-p14	"NAD(P)H dehydrogenase, quinone 1"
	BC000906.1	NQO1	6118	0	3.61596	16q22.1	claudin 10
	NM_006984.1	CLDN10	7155	1E-08	3.842393	13q31-q34	"aldo-keto reductase family 1, member C1 (dihydrodiol dehydrogenase 1; 20-alpha (3-alpha)-hydroxysteroid dehydrogenase)"
	S68290.1	AKR1C1	6805	3.8E-07	3.859724	10p15-p14	"aldo-keto reductase family 1, member C1 (dihydrodiol dehydrogenase 1; 20-alpha (3-alpha)-hydroxysteroid dehydrogenase)"
	M33376.1	AKR1C2		9E-08	4.050088	10p15-p14	"aldo-keto reductase family 1, member C2 (dihydrodiol dehydrogenase 2; bile acid binding protein; 3-alpha hydroxysteroid dehydrogenase, type III)"
	NM_002083.1	GPX2	6979	0	4.247676	14q24.1	glutathione peroxidase 2 (gastrointestinal)
	NM_000903.1	NQO1	6118	0	4.278763	16q22.1	"NAD(P)H dehydrogenase, quinone 1"
	NM_000691.1	ALDH3A1	6081	0	7.135677	17p11.2	"aldehyde dehydrogenase

FIG. 11
(cont'd.)

209351_at	BC002690.1	KRT14	7148	0.00058	2.8239	17q12-q21	NADP(+)-dependent, cytosolic"
209386_at	AI346835	TM4SF1	5887	0.00012	2.998073	3q21-q25	"keratin 14 (epidermolysis bullosa simplex, Dowling-Meara, Koebner)"
							transmembrane 4
							superfamily member 1
							"aldo-keto reductase family 1, member C1 (dihydrodiol dehydrogenase 1; 20-alpha (3-alpha)-hydroxysteroid dehydrogenase)"
	NM_001353.2	AKR1C1	6805	2.9E-05	3.186574	10p15-p14	"NAD(P)H dehydrogenase, quinone 1"
	BC000906.1	NQO1	6118	0	3.61596	16q22.1	claudin 10
	NM_006984.1	CLDN10	7155	1E-08	3.842393	13q31-q34	"aldo-keto reductase family 1, member C1 (dihydrodiol dehydrogenase 1; 20-alpha (3-alpha)-hydroxysteroid dehydrogenase)"
	S68290.1	AKR1C1	6805	3.8E-07	3.859724	10p15-p14	member C2 (dihydrodiol dehydrogenase 2; bile acid binding protein; 3-alpha hydroxysteroid dehydrogenase, type III)"
	M33376.1	AKR1C2		9E-08	4.050088	10p15-p14	glutathione peroxidase 2 (gastrointestinal)
	NM_002083.1	GPX2	6979	0	4.247676	14q24.1	"NAD(P)H dehydrogenase, quinone 1"
	NM_000903.1	NQO1	6118	0	4.278763	16q22.1	"aldehyde dehydrogenase
	NM_000691.1	ALDH3A1	6081	0	7.135677	17p11.2	

FIG. 11
(cont'd.)

NM_004363.1	CEACAM5	5887	1.5E-05	7.574469	19q13.1-q13.2	3 family, member A1" carcinoembryonic antigen-related cell adhesion molecule 5 "cytochrome P450, family 1, subfamily B, polypeptide 1" "aldo-keto reductase family 1, member B10 (aldose reductase)"
202435_s_at	CYP1B1	6118	3.6E-05	8.874184	2p21	
206561_s_at	AKR1B10	4033	0.0005	25.99183	7q33	

FIG. 11
(cont'd.)

Affymetrix	GENBANK	HUGO	GO	Smoker/ Non-smoker	Smoker/ Non-Smoker Expression Ratio
ID	ID	ID	ID	p-value	
205680_at	NM_002425	MMP10	30574	4E-08	0.397067
210524_x_at	NM_007372	MT1F	5737	7.81E-06	0.527231
208581_x_at	NM_005952	MT1X	9634	3.1E-07	0.553203
211538_s_at	NM_021979	HSPA2	7286	1.6E-07	0.594697
204745_x_at	NM_005950	MT1G	46872	1.47E-06	0.600768
217165_x_at	M10943	MT1F	5737	3.1E-07	0.617346
221016_s_at	NM_031283	TCF-3	6355	1.9E-07	0.69786
211026_s_at	NM_007283	MGLL	6954	6.72E-06	0.757342
200599_s_at	NM_003299	TRA1	5524	1.6E-06	1.28607
200863_s_at	NM_004663	RAB11A	6886	1.51E-05	1.287348
201923_at	NM_006406	PRDX4	7252	1.46E-05	1.31812
208918_s_at	NM_023018	FLJ13052		1.63E-05	1.357851
208919_s_at	NM_023018	FLJ13052		2.38E-06	1.377841
202481_at	NM_004753	SDR1	8152	3.25E-06	1.386494
204500_s_at	NM_015239	AGTPBP1		1.73E-05	1.434528
206302_s_at	NM_019094	NUDT4	9187	9.8E-07	1.438227
200748_s_at	NM_002032	FTH1	6826	0	1.482301
203397_s_at	NM_004482	GALNT3	5975	1.25E-05	1.494527
214106_s_at	NM_001500	GMDS	5975	6.9E-07	1.505996
201263_at	NM_003191	TARS	6435	2.06E-05	1.534493
204970_s_at	NM_002359	MAFG	6355	1.06E-05	1.54913
200872_at	NM_002966	S100A10	7165	1.83E-05	1.599726
208680_at	NM_002574	PRDX1	8283	4.2E-07	1.624891
218313_s_at	NM_017423	GALNT7	5975	1.1E-07	1.636258
201431_s_at	NM_001387	DPYSL3	7165	5E-07	1.7288
217755_at	NM_016185	HNI		2E-08	1.732046
203963_at	NM_001218	CA12	6730	5.4E-07	1.751505

FIG. 12

202923_s_at	NM_001498	GCLC	6534	1.7E-07	1.773281
204875_s_at	NM_001500	GMDS	5975	8E-08	1.830569
201266_at	NM_003330	TXNRD1	6118	3E-08	1.865058
201118_at	NM_002631	PGD	9051	2.3E-07	1.866207
209369_at	NM_005139	ANXA3	5737	2.5E-07	1.872862
203925_at	NM_002061	GCLM	6534	1.54E-06	1.87522
211657_at	M18728.1	CEACAM6	7165	2E-08	1.925775
208864_s_at	NM_003329	TXN	7165	0	1.961322
201463_s_at	NM_006755	TALDO1	5975	0	1.974839
203757_s_at	NM_002483	CEACAM6	7165	1.65E-06	1.987336
205499_at	NM_014467	SRPUL	6118	3E-08	2.038793
204341_at	NM_006470	TRIM16	5737	0	2.048029
204058_at	AL049699	ME1	6099	0	2.104857
221841_s_at	NM_004235	---		9.18E-06	2.208524
204059_s_at	NM_002395	ME1	6099	0	2.414563
204151_x_at	NM_001353	AKR1C1	6805	2.93E-06	2.854519
210519_s_at	BC000906.1	NQO1	6118	0	3.076752
216594_x_at	S68290.1	AKR1C1	6805	3E-08	3.372689
202831_at	NM_002083	GPX2	6979	0	3.429494
205328_at	NM_006984	CLDN10	7155	0	3.432973
201468_s_at	NM_000903	NQO1	6118	0	3.467371
201467_s_at	NM_000903	NQO1	6118	0	4.008402
209699_x_at	NM_001354	AKR1C2	15722	1.6E-07	4.214368
217626_at	BF508244	AKR1C1	6805	8E-08	5.286915
205623_at	NM_000691	ALDH3A1	6081	0	6.067625
202435_s_at	NM_000104	CYP1B1	6118	9.61E-06	7.096588
202436_s_at	NM_000104	CYP1B1	6118	2.96E-06	14.65085
202437_s_at	NM_000104	CYP1B1	6118	5.5E-07	25.18444

FIG. 12
(cont'd.)